





Qy	153	-----	ProGlnAlaGluProValTrpThrProPro---	162
		:::	:	
Db	133	ACGGGGCTGGCCGGGTTGGCTTCCGGACAGAACAGAGCTGGTCCAGGT		74
Qy	163	-----	AlaProAlaProAlaAlaProProSerThr	172
		:::	:	
Db	73	CTTCCATGGCTGGAGGTGGATGATGCGCAGCTGCAGCTGCCGGCCCGCG		14
Qy	173	Ser 173		
Db	13	TCT 11		

Search completed: June 22, 2005, 09:17:30  
Job time : 2 secs

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	673	GCCGGCCCTCCCTCCTCCCCGCAAGCTGCCCCAGGCCAGCGAGCCGTGGANC	732	Db	1753	GAAGGCCAAATAGTAAAGAGAACTAGCACCAAAACATCAAACCCCTTTACTTG	1812
Qy	161	ProProAlaProAlaAlaProProSerThrProAlaAlaProlysArgArgCly	180	Oy	506	alAlaAlaGlnDaspSergluThrAspTyrValThrAspAsnLeuThrLysValThrG	526
Db	733	CCGGCAGGCCGGCTNCCCACGCCGCCCCCTCACCACGCCAACGGCC	792	Db	1813	TACCGACAGGATTCTGAGCACAGATTGTCACAAGATTAACAAAGGTGACTG	1872
Qy	181	SerSerGlyAla-----	186	Qy	526	IuGlutAlaAlaAsnMetProGluGlyLeuThrProAspLeuValGlnGluAlaCysG	546
Db	793	TCTCTGGGGTCAGGGATAAGACCTTTGCTCTCTCTGAGCTGTGATA	852	Db	1873	AGGAGTGTGGCAAAATGCGCTGAACGCCCTGACTCCGAGTGTAGAACAGCATG	1932
Qy	187	*****LysIleMetAspLeuLysGluGlnProGlyAsnThrIleSerAlaCly	206	Qy	546	IuSerGluLeuAsnGluValThrGlyIuLysAlaItyGluThrLysMetAspLeuV	566
Db	853	CGCTCCTGCAAGAAAATGGACTGAGGGAGCAGCTGAGGGTAACTATTCGGCTG	912	Db	1933	AAGTGAATGATGAACTTACTGGTACAAAGTTGCTTAAACAAATGGCATCTGG	1992
Qy	207	GlnGluAspPheProSerValLeuGluThrAlaAlaSer***ProSerIeuSerPro	226	Qy	566	alGlnThrSerGluValMetGlnDluSerLeuTyriProAlaAlaGlnLeuCysProSerP	586
Db	913	CAAGGGATTCCATCTCCTCCTGAAACTGCTGCTCTCTGTCCTCTCTCTCT	972	Db	1993	TTCAAACATCAGAGGTTGACTCTATCCGAGCAGCTGTTGCCATCAT	2052
Qy	227	LeuSerAlaAlaSerPheIleSerGluHiSglutYrLeuGlyAsnLeuSerThrValPro	246	Qy	586	heGluGluSerGluAlaIthrProSerProValLeuProAspLeuValMetGluAlaApol	606
Db	973	CTCTCAGCCGCTCTTCTGAAAGCATGATACTTGAAATTGCTGAACTATTAC	1032	Db	2053	TTCAGAAGCTCAGAGCTACTCTTCAACAGTTTGCTGACATTGTGAAAGCACCAT	2112
Qy	247	ThrGluGlyThrIleLeuGlnGluAsnValSerGluAlaSerLysLeuGlyAsnLeuSerThrValPro	266	Qy	606	euhAsnSerAlaValProSerAlaGlyAlaSerValIleLeuGlnProGluAsnProProProtYRG	646
Db	1033	ACTGAGGAAACCTCAAGAAAATGTCACTGAGCTTAAGGGTCACTGAGCTAAAGCA	1092	Db	2173	AAGCTCTTCAGTTCACTGAAATTGAAAGCTAAACATGAGCTGAAACCCCACCATG	2232
Qy	267	LysThrLeuIleIleAspArgAspLeuThrGluPheSerGluLeuGluThrSerGluMet	286	Qy	646	IuGluIaMetSerValSerIleLeu---LysValSerGlyIleLeuGluGluLeuGluP	665
Db	1093	AAAACTCTACTCATAGATAGAGATTAAAGAGTTAACAGAGTTAACATGAAATG	1152	Db	2233	AAGAGGCCATGACTGTATCACTAAAAAGTAGTCAAGGAAATAAGGAAATAAGAGC	2292
Qy	287	GlySerSerPheSerValSerGluAlaSerAlaValLeuAlaAsnProAla	306	Db	655	roGluAsnIleAsnAlaLeuGlnGluAlaProTyrylSerIleAlaCysA	685
Db	1153	GGATCATCCTTCACTGTCTCTCAGTGGTAACTAGCTGAAATCCTAG	1212	Qy	2293	CTGAAAAATTATGAGCTCTTCATCAAGAACAGAGCTCCTTATATCTATCTATGCTGCTG	2352
Qy	307	GlugluIleIleValLysAsnBspGluGluGluLysLeuValSerAlaSerAlaIleu	326	Db	685	spleuIleLeuGluThrLysLeuSerAlaGluProAlaProAspPhaserAspYrSerG	705
Db	1213	GAAGAAATATCGTAAAAAATAAGATGAGAAAGAGTTACTTGTAAAGTAGT	1272	Qy	705	luMetAlaIleValGluGluInProValProAspHisSerGluLeuValGluAspSerP	725
Qy	327	His***GlnGlnGluLeuProThrAlaLeuThrAlaLeuThrAlaLeuThrAlaLeu	346	Db	2353	ATTATTAAGAACAAAGCTTCTGTGAACTGCTGATCTGAGCTGTTGATTCAGT	2412
Db	1273	CATAATCACAAAGTTACCTACAGCTCTACTAAAGTTAACAGGATGAGTTG	1332	Qy	2413	AAATGGCAAAGGTGAAAGCAGCTGAGCTGCTGATCTGAGCTGTTGATTCCTC	2472
Qy	347	SerSerGlyAlaAlaLysAspSerPheAsnGluLysArgValAlaValGluAlaProMet	366	Db	725	roAspSerGluProValAspLeuPheSerAspAspSerIleProGlnValProGlnLySG	745
Db	1333	TCTTCAGAAAGAAAAGACAGTTAAATGAAAGAGAGTTGAACTGCTCATG	1392	Qy	2553	AAGATGAAACTGTGTTGAAAGAAAGTCTGACCTTCACAAAGATAACAAAAAC	2592
Qy	367	ArgGluGlyUtyAlaAspHelysProPheGluArgValTrpGluValLysAspSerLys	386	Db	2473	CTGATTCGAAACAGTGACTTATGATGATGATTCATCTGACCTTCACAAAGAA	2532
Db	1393	AGGGAGGATATGCAGACTCAACCATTGAGACTCAAAGTGTAGTAG	1452	Qy	745	InaspGluThrValMetLeuValLysGluSerIleLeuSerThrGluSerMetI	765
Qy	387	GluAspSerAspMetLeuAlaAlaGlyGlyLysIleGluSerAsnLeuGluSerLysVal	406	Db	2593	TAGATAAGAAATAAGAAAALACTGCTGACCTGAGGAGAAAGCCATA	2652
Db	1453	GAAGATGAGTAGTATACTGCTGAGGTAAATATCGAGGAACTTGAAAGTGA	1512	Qy	785	euGluSerPheAspLeuSerLeuAspPheIleSerLysAspThrLeuProAspGluIvals	805
Qy	407	AspLysLysCysPheAlaLysAspSerPheAsnProAlaAlaSerGlyLysIleGluSerIleAlaThrAsnIlePhe	426	Db	2653	TGAAATCTTTAAAGCTCAAGTTAGATAACAAAGATAACAAAGATAACAA	2712
Db	1513	GATAAAATGTTGCAAGATAACCGAGTAACTATCAGCAAAACTAAAGATACTG	1572	Qy	805	erThrLeuSerLysIleGluLysIleLeuSerAlaLeuSerThrAlaValT	825
Qy	427	SerAsnAspSerAspThrSerIleProSerThrProGluGlyLysIleGluSerGlyAla	446	Db	2713	CAACATGAGCTTTCAGGAGAAATTCTTTCAGGAGCTAGTACTGCAAGTT	2772
Db	1573	AGTATGATGATGACTCTTCCCCAGTACGCCAGAAAGGTATAGGTGTTAGGAGCA	1632	Qy	825	YrSerAspAspSerPheIleSerLysIleLeuSerAlaGlnIleArgGluThrPheS	845
Qy	447	TyrIleThrCysAlaProHeAsnProAlaAlaThrGluSerIleAlaThrAsnIlePhe	466	Db	2773	ATTCAAAATGATGACTTATCTAGGAGCAAGTAAAGAAACTGAAACGTTT	2832
Db	1633	TATTCACATGTTGAGAGATCCCTTAACCGAGGAACTGAGGCAATGAAACATTT	1692	Qy	845	erAspSerSerProIleGluLileAspGluPheProThrLeuIleSerSerLysThrA	865
Qy	467	ProLeuGluAspProThrSerGluAsn**ThrAspGlu-LysIleGluGlu	486	Db	2833	CAAGTCATCTCCAAATTATGAGCTTCACTGAACTTCATGAACTGTTAAACTG	2892
Db	1693	CCTTTGTTAGGAGATCCCTTAACGAAATAAGCCATGAACTGAGGCAATGAA	1752	Qy			
Qy	486	SlyLeuAlaGlnIleValThrGluLysAsnThrSerThrSerLysProhe-PheV	506	Db			

865 spSerPheSerLysLeuAlaArgGlutyrThrAspIeuGluValSerHisLysSerGluI 885  
 Db 2893 ATTCAATTCTAAATTAGCCGGATATACTGACTAGAGTATGCCAAACTGAA 2952  
 ; DT 27-NOV-2002 (first entry)  
 ; XX Human bone remodelling gene #106.  
 ; DE ; XX  
 ; KW Bone remodelling; osteoporosis; human; gene; 88.  
 ; OS ; XX  
 ; Homo sapiens.  
 ; PN US6426186-B1.  
 ; XX  
 ; PD 30-JUL-2002.  
 ; XX  
 ; PF 18-JAN-2000; 2000US-00484970.  
 ; XX  
 ; PR 18-JAN-2000; 2000US-00484970.  
 ; XX  
 ; PA (INCY-) INCYTE GENOMICS INC.  
 ; P1 Jones KA, Volkhardt W, Walker MG;  
 ; P2 XX  
 ; DR WPT; 2002-673014/72.  
 ; XX  
 ; PT A combination of polynucleotides which are co-expressed with genes known  
 ; PT to be involved in bone remodeling and osteoporosis are useful in an array  
 ; PT for the diagnosis of bone remodeling and osteoporosis associated  
 ; PT disorders.  
 ; XX  
 ; Claim 1; Col 283-288; 206pp; English.  
 ; XX  
 ; CC The invention relates to a combination comprising a number of  
 ; CC substantially purified and isolated polynucleotides which are co-  
 ; CC expressed with genes known to be involved in bone remodelling and  
 ; CC osteoporosis. The invention is used to diagnose disorders associated with  
 ; CC bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone  
 ; CC remodelling genes of the invention.  
 ; XX  
 ; SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;  
 ; ABS70449 Length: 4822 June 22, 2005 09:05 Type: N Check: 9399 ..  
 ; ABS70449

Alignment Scores:  
 Pred. No.: 0 Length: 4822  
 Score: 96.00 Matches: 42  
 Percent Similarity: 31.93% Conservative: 11  
 Best Local Similarity: 25.30%  
 Query Match: 1.62% Indels: 52  
 DB: 1 Gaps: 7

US-09-830-972-29-COPY (1-1178) x abs70449 (1-4822)

Qy 1005 ValValPheGlyAlaSerLeuIleLeuLeuSerLeuIrrValPheSerIleValSer 1024  
 Db 3310 GTGGGTTGGTGTGGCCAGGCTATTCCCTGGCTTCATTGACGATTACACATTGAC 3369  
 ; Qy 1025 ValThrAlaValLeuIleAlaLeuIleAlaLeuIleValLeuIleValLeuIleVal 1044  
 Db 3370 GAAACGCCATTACATGGCTGCCCTCTCTGACCATCTGCTTAGATATACAG 3429  
 ; Qy 1045 GlyValIleGlnAlaLeuGlnLysSerAspGluGlyHisProPheArgAlaTyrlieGlu 1064  
 Db 3430 GGTGATCAGCTAACCTGGCCACCACTGGATATCGAA 3489  
 ; Qy 1065 SerGluValAlaLeuIleSerGluLeuValGlnLysTrpSerAsnSerAlaLeuGlyHis 1084  
 Db 3490 TCTGAAGTGTCTATCTGAGAAGTGTCTGAAACTACATAATCTGCCTCTGCTCAT 3549  
 ; Qy 1085 ValAlanylSThrIleGluLeuIleSerLeuIleValAspIleLeuIleValAspSer 1104  
 Db 3550 GTGAACCTGACCATAAAGGAACCTCGGCCCTCTCTGACCATCTGCTTAGATGCTATTGCT 3609  
 ; Qy 1105 LeuLysPheAlaValIleMetTrpValPhenIrrValGlyAlaLeupheAsnGlyLeu 1124  
 Db 3610 CTGAAGTTGCAAGTGTCTATCTGCTGCTGCTGTTGCTGCTGCTGCTGCTG 3669  
 ; Qy 1125 ThrIleLeuIleLeuAlaIleSerLeuIleSerValProValIleTrpGluArgHis 1144  
 Db 3670 ACACATGCTTGTCTCATTTCTACCTCTGCTTCTGTTCTGTTCTGTTCTGCT 3729  
 ; Qy 1145 GluAlaIleAspHsTyrIleGluLeuIleAspHsTyrIleGluLeuIleAspHsTyr 1164  
 Db 3730 CAGGCACTGATGATCATTAATCTGACTCTGAAATAGATGTTAAAGATGCTATGGCT 3789  
 ; Qy 1165 LysIleGlnAlaLysIlePheProGlyLeuIleArgLysAlaGlu 1178  
 Db 3790 AAAATCCAAGAAAAATCCCTGAAGGCAANGCTGAA 3831  
 ; Qy 89 AlaProArgGlyProIleProAlaAlaProProAlaProAlaProAlaProAlaPro 102  
 ; Db 556 GGGCGGGGGGGAGGGGGAGGGGGCTCCGGGGCGGGGGCGACGAAAGTCATTTC 497  
 ; Qy 103 -----GluArgGlnProSerTrpAspProSerProValSerSer 115  
 ; Db 496 CGAAGTGCATTANNGGGCGCCGCGCAGGGGGACTGCGGCGGACTGCGGCGGCC 437  
 ; Qy 116 ThrValProAlaProSerProLeuSerAlaAlaValSerProSerLysIleProGlu 135

RESULT 2  
 abs70449/c : TOIG of: abs70449 check: 9399 from: 1 to: 4822  
 ; ID ABS70449 standard; CDNA; 4822 BP.  
 ; XX  
 ; AC  
 ; AC ABS70449;  
 ; XX

Search completed: June 22, 2005, 09:12:28  
Job time: 23 secs